

clones were sequenced and ordered to arrive at a complete sequence for GLUTX. The nucleotide sequence of GLUTX is shown in [Fig. 1] Figs. 1A-1E. The predicted amino acid sequence of GLUTX is also shown in [Fig. 2] Figs. 2A-2D.

Second paragraph on page 82 at about lines 13-27:

The predicted amino acid sequence of GLUTX was compared to the amino acid sequences of GLUT1, (SEQ ID NO:3), GLUT2 (SEQ ID NO:4), GLUT3 (SEQ ID NO:5), GLUT4 (SEQ ID NO:6), and GLUT5 (SEQ ID NO:7). This comparison is depicted in [Fig. 3] Figs. 3A-3D along with a majority sequence (SEQ ID NO:8). As noted above, in designing variant forms of GLUTX which retain the activity of wild-type GLUTX, it is generally preferable to avoid altering residues that are highly conserved. Of course, if one wished to design a reduced activity variant of GLUTX, it is generally preferable to alter conserved residues. Using sequence comparison information one can design GLUTX variants which are more similar to GLUT1, (SEQ ID NO:3), GLUT2 (SEQ ID NO:4), GLUT3 (SEQ ID NO:5), GLUT4 (SEQ ID NO:6), or GLUT5 (SEQ ID NO:7).